

SEQUENCE LISTING

5 <110> Degussa AG
 National University of Ireland, Galway
 Forschungszentrum Jülich GmbH

10 <120> Process for the Preparation of L-Amino Acids with
 Amplification of the zwf Gene.

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 Gln Val Asp Ile Asn Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys
 290 295 300
 50 Tyr Pro Val Thr Gly Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro
 305 310 315 320
 His Val Lys Glu Lys Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys
 325 330 335
 55 Ala His Glu Arg Lys Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn
 340 345 350

Val Glu Lys His Val Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu
355 360 365

5 Asn Glu Leu Ala Asp Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met
370 375 380

Cys Asn Val Trp His Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg
385 390 395 400

10 Asp Phe Val Gly Ser Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro
405 410 415

His Ala Ile Gly Ala Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala
420 425 430

15 Met Cys Gly Asp Gly Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr
435 440 445

20 Val Lys Leu His Gln Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser
450 455 460

Ser Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu
465 470 475 480

25 Phe Gly Thr Asp His Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala
485 490 495

Ala Gly Ile Lys Ser Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu
500 505 510

30 Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile
515 520 525

35 Val Thr Asp Pro Asn Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu
530 535 540

Gln Val Met Gly Phe Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly
545 550 555 560

40 Gly Val Gly Ala Met Ile Asp Leu Ala Arg Ser Asn Ile Arg Asn Ile
565 570 575

Pro Thr Pro

45

<210> 6
<211> 875
50 <212> DNA
<213> *Corynebacterium glutamicum*

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accatggcgg gtaaaaggtgt gtcggtggta gtgattcctg gtgatatcgc taaggaagac 120
cgaggtgacg gtacttattc caattccact atttctctg gcactcctgt ggtgttccc 180
gatcctactg aggctgcagc gctggtggag gcgattaaca acgctaagtc tgtcactttg 240
ttctgcggtg cgggcgtgaa gaatgctcgc gcgcaggtgt tggagtgagg ggagaagatt 300
aaatcaccga tcgggcatgc gctgggtggt aagcagtaca tccagcatga gaatccgttt 360

gaggtcgccga tgtctggcct gcttgggttac ggcgcctcg tggatgcgt caatgaggcg 420
 gatctgctga ttctattggg tacggatttc ccttattctg atttccttc taaagacaac 480
 gttgccccagg tggatatcaa cggtcgcgac attggtcgac gtaccacggt gaagtatccg 540
 5 gtgaccggtg atgttgctgc aacaatcgaa aatatcttgc ctcattgtgaa ggaaaaaaca 600
 gatcgttctt tccttgatcg gatgtctcaag gcacacgagc gtaagttgag ctccgttggtg 660
 gagagctaca cacataacgt cgagaagcat gtgcctatcc accctgaata cgttgccctct 720
 attttgaacg agctggcgga taaggatgcy gtgtttactg tggataccgg catgtgcaat 780
 gtgtggcatg cgaggtacat cgagaatccg gagggaaacgc gcgactttgt ggggttcattc 840
 10 cgccacggca cgatggctaa tgcgttgccct catgc 875

<210> 7

<211> 2260

<212> DNA

15 <213> *Brevibacterium flavum* MJ-233

<220>

<221> CDS

<222> (629)..(2080)

20 <223> Glucose-6-Phosphate Dehydrogenase (EC 1.1.1.49);
JP-A-09-22461

<400> 7

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 acgctgtgta caaggagctt ttcgacgccg ccgagctgcc tgtaaggcgc caaactcag 120
 cgcccaactgt gggcatccac cggcgtgaag aaccctgcgt acgctgcaac tctttacgtt 180
 30 tccgagctgg ctgggtccaaa caccgtcaac accatgccag aaggcaccat cgacgctggt 240
 ctggaactgg gcaacctgca cggtgacaac ctgtccaact ccgcgcgcaga agctgacgct 300
 35 gtgttctccc agcttgaggc tctggggcgt gacttggcag atgtcttcca ggtcctggag 360
 accgaggcgc tggacaagtt cggtgtcttc tggagcgaac tgcttgagtc catggaagct 420
 cgctgaagt agaactagca cgctgcatca gtaacggcga catgaaatcg aattagttcg 480
 40 atcttatgtg gccgttacac atctttcatt aaagaaagga tcgtgacgct taccatcgtg 540
 agcacaaaaa acgaccccct ccagctggac aaacccactg cgcgaccgcg aggataaacg 600

45 actccccgc atcgtgggcc ctccggcg atg gtg atc ttc ggt gtc act ggc 652
 Met Val Ile Phe Gly Val Thr Gly
 1 5

50 gac ttg gct cga aag aag ctg etc ccc gcc att tat gat cta gca aac 700
 Asp Leu Ala Arg Lys Lys Leu Leu Pro Ala Ile Tyr Asp Leu Ala Asn
 10 15 20

cgc gga ttg ctg ccc cca gga ttc tog ttg gta ggt tac ggc cgc cgc 748
 Arg Gly Leu Leu Pro Pro Gly Phe Ser Leu Val Gly Tyr Gly Arg Arg
 25 30 35 40

55 gaa tgg tcc aaa gaa gac ttt gaa aaa tac gta cgc gat gcc gca agt 796
 Glu Trp Ser Lys Glu Asp Phe Glu Lys Tyr Val Arg Asp Ala Ala Ser
 45 50 55

	gct ggt gct cgt acg gaa ttc cgt gaa aat gtt tgg gag cgc ctc gcc	844
	Ala Gly Ala Arg Thr Glu Phe Arg Glu Asn Val Trp Glu Arg Leu Ala	
	60 65 70	
5	gag ggt atg gaa ttt gtt cgc ggc aac ttt gat gat gca gct ttc	892
	Glu Gly Met Glu Phe Val Arg Gly Asn Phe Asp Asp Ala Ala Phe	
	75 80 85	
10	gac aac ctc gct gca aca ctc aag cgc atc gac aaa acc cgc ggc acc	940
	Asp Asn Leu Ala Ala Thr Lys Arg Ile Asp Lys Thr Arg Gly Thr	
	90 95 100	
15	gcc ggc aac tgg gct tac tac ctg tcc att cca cca gat tcc ttc gca	988
	Ala Gly Asn Trp Ala Tyr Leu Ser Ile Pro Asp Ser Phe Ala	
	105 110 115 120	
20	gcg gtc tgc cac cag ctg gag cgt tcc ggc atg gct gaa tcc acc gaa	1036
	Ala Val Cys His Gln Leu Glu Arg Ser Gly Met Ala Glu Ser Thr Glu	
	125 130 135	
25	gaa gca tgg cgc cgc gtg atc atc gag aag cct ttc ggc cac aac ctc	1084
	Glu Ala Trp Arg Arg Val Ile Ile Glu Lys Pro Phe Gly His Asn Leu	
	140 145 150	
30	gaa tcc gca cac gag ctc aac cag ctg gtc aac gca gtc ttc cca gaa	1132
	Glu Ser Ala His Glu Leu Asn Gln Leu Val Asn Ala Val Phe Pro Glu	
	155 160 165	
35	tct tct gtg ttc cgc atc gac cac tat ttg ggc aag gaa aca gtt caa	1180
	Ser Ser Val Phe Arg Ile Asp His Tyr Leu Gly Lys Glu Thr Val Gln	
	170 175 180	
40	aac atc ctg gct ctg cgt ttt gct aac cag ctg ttt gag cca ctg tgg	1228
	Asn Ile Leu Ala Leu Arg Phe Ala Asn Gln Leu Phe Glu Pro Leu Trp	
	185 190 195 200	
45	aac tcc aac tac gtt gac cac gtc cag atc acc atg gct gaa gat att	1276
	Asn Ser Asn Tyr Val Asp His Val Gln Ile Thr Met Ala Glu Asp Ile	
	205 210 215	
50	ggc ttg ggt gga cgt gct ggt tac tac gac ggc atc ggc gca gcc cgc	1324
	Gly Leu Gly Gly Arg Ala Gly Tyr Tyr Asp Gly Ile Gly Ala Ala Arg	
	220 225 230	
55	gac gtc atc cag aac cac ctg atc cag ctc ttg gct ctg gtt gcc atg	1372
	Asp Val Ile Gln Asn His Leu Ile Gln Leu Leu Ala Leu Val Ala Met	
	235 240 245	
60	gaa gaa cca att tct ttc gtg cca cgc cag ctg cag gca gaa aag atc	1420
	Glu Glu Pro Ile Ser Phe Val Pro Ala Gln Leu Gln Ala Glu Lys Ile	
	250 255 260	
65	aag gtg ctc tct gcg aca aag ccg tgc tac cca ttg gat aaa acc tcc	1468
	Lys Val Leu Ser Ala Thr Lys Pro Cys Tyr Pro Leu Asp Lys Thr Ser	
	265 270 275 280	
70	gct cgt ggt cag tac gct gcc ggt tgg cag ggc tct gag tta gtc aag	1516
	Ala Arg Gly Gln Tyr Ala Ala Gly Trp Gln Gly Ser Glu Leu Val Lys	
	285 290 295	

	gga ctt cgc gaa gaa gat ggc ttc aac cct gag tcc acc act gag act	1564
	Gly Leu Arg Glu Glu Asp Gly Phe Asn Pro Glu Ser Thr Thr Glu Thr	
	300 305 310	
5	ttt gcg gct tgt acc tta gag atc acg tct cgt cgc tgg gct ggt gtg	1612
	Phe Ala Ala Cys Thr Leu Glu Ile Thr Ser Arg Arg Trp Ala Gly Val	
	315 320 325	
10	cgc ttc tac ctg cgc acc ggt aag cgt ctt ggt cgc cgt gtt act gag	1660
	Pro Phe Tyr Leu Arg Thr Gly Lys Arg Leu Gly Arg Val Thr Glu	
	330 335 340	
15	att gcc gtg gtg ttt aaa gac gca cca cac cag cct ttc gac ggc gac	1708
	Ile Ala Val Val Phe Lys Asp Ala Pro His Gln Pro Phe Asp Gly Asp	
	345 350 355 360	
	atg act gta tcc ctt ggc caa aac gcc atc gtg att cgc gtg cag cct	1756
	Met Thr Val Ser Leu Gly Gln Asn Ala Ile Val Ile Arg Val Gln Pro	
	365 370 375	
20	gat gaa ggt gtg ctg atc cgc ttc ggt tcc aag gtt cca ggt tct gcc	1804
	Asp Glu Gly Val Leu Ile Arg Phe Gly Ser Lys Val Pro Gly Ser Ala	
	380 385 390	
25	atg gaa gtc cgt gac gtc aac atg gac ttc tcc tac tca gaa tcc ttc	1852
	Met Glu Val Arg Asp Val Asn Met Asp Phe Ser Tyr Ser Glu Ser Phe	
	395 400 405	
30	act gaa gaa tca cct gaa gca tac gag cgc ctt atc ttg gat gcg ctg	1900
	Thr Glu Glu Ser Pro Glu Ala Tyr Glu Arg Leu Ile Leu Asp Ala Leu	
	410 415 420	
35	ttg gat gaa tcc agc ctt ttc cct acc aac gag gaa gtg gaa ctg agc	1948
	Leu Asp Glu Ser Ser Leu Phe Pro Thr Asn Glu Glu Val Glu Leu Ser	
	425 430 435 440	
	tgg aag att ctg gat cca att ctt gaa gca tgg gat gcc gat gga gaa	1996
	Trp Lys Ile Leu Asp Pro Ile Leu Glu Ala Trp Asp Ala Asp Gly Glu	
	445 450 455	
40	cca gag gat tac cca gca ggt acg tgg ggt cca aag agc gct gat gaa	2044
	Pro Glu Asp Tyr Pro Ala Gly Thr Trp Gly Pro Lys Ser Ala Asp Glu	
	460 465 470	
45	atg ctt tcc cgc aac ggt cac acc tgg cgc agg cca taatttaggg	2090
	Met Leu Ser Arg Asn Gly His Thr Trp Arg Arg Pro	
	475 480	
50	gcaaaaaatg atctttgaac ttccggatgc caccacccag caaatttcca agaccctaac	2150
	tcgactgcgt gaatcggggca cccaggtcac caccggccga gtgctcacc tcactgtggt	2210
	cactgactcc gaaagcgatg tcgctgcagt taccgagtc accaatgaag	2260
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<210> 8
 <211> 484
 <212> PRT

<213> Brevibacterium flavum MJ-233

<400> 8

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 Pro Ala Ile Tyr Asp Leu Ala Asn Arg Gly Leu Leu Pro Pro Gly Phe
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 10 Ser Leu Val Gly Tyr Gly Arg Arg Glu Trp Ser Lys Glu Asp Phe Glu
 35 40 45
 Lys Tyr Val Arg Asp Ala Ala Ser Ala Gly Ala Arg Thr Glu Phe Arg
 50 55 60
 15 Glu Asn Val Trp Glu Arg Leu Ala Glu Gly Met Glu Phe Val Arg Gly
 65 70 75 80
 20 Asn Phe Asp Asp Asp Ala Ala Phe Asp Asn Leu Ala Ala Thr Leu Lys
 85 90 95
 Arg Ile Asp Lys Thr Arg Gly Thr Ala Gly Asn Trp Ala Tyr Tyr Leu
 100 105 110
 25 Ser Ile Pro Pro Asp Ser Phe Ala Ala Val Cys His Gln Leu Glu Arg
 115 120 125
 Ser Gly Met Ala Glu Ser Thr Glu Glu Ala Trp Arg Arg Val Ile Ile
 130 135 140
 30 Glu Lys Pro Phe Gly His Asn Leu Glu Ser Ala His Glu Leu Asn Gln
 145 150 155 160
 35 Leu Val Asn Ala Val Phe Pro Glu Ser Ser Val Phe Arg Ile Asp His
 165 170 175
 Tyr Leu Gly Lys Glu Thr Val Gln Asn Ile Leu Ala Leu Arg Phe Ala
 180 185 190
 40 Asn Gln Leu Phe Glu Pro Leu Trp Asn Ser Asn Tyr Val Asp His Val
 195 200 205
 Gln Ile Thr Met Ala Glu Asp Ile Gly Leu Gly Gly Arg Ala Gly Tyr
 210 215 220
 45 Tyr Asp Gly Ile Gly Ala Ala Arg Asp Val Ile Gln Asn His Leu Ile
 225 230 235 240
 50 Gln Leu Leu Ala Leu Val Ala Met Glu Glu Pro Ile Ser Phe Val Pro
 245 250 255
 Ala Gln Leu Gln Ala Glu Lys Ile Lys Val Leu Ser Ala Thr Lys Pro
 260 265 270
 55 Cys Tyr Pro Leu Asp Lys Thr Ser Ala Arg Gly Gln Tyr Ala Ala Gly
 275 280 285
 Trp Gln Gly Ser Glu Leu Val Lys Gly Leu Arg Glu Glu Asp Gly Phe
 290 295 300

Asn Pro Glu Ser Thr Thr Glu Thr Phe Ala Ala Cys Thr Leu Glu Ile
 305 310 315 320
 5 Thr Ser Arg Arg Trp Ala Gly Val Pro Phe Tyr Leu Arg Thr Gly Lys
 325 330 335
 Arg Leu Gly Arg Arg Val Thr Glu Ile Ala Val Val Phe Lys Asp Ala
 340 345 350
 10 Pro His Gln Pro Phe Asp Gly Asp Met Thr Val Ser Leu Gly Gln Asn
 355 360 365
 Ala Ile Val Ile Arg Val Gln Pro Asp Glu Gly Val Leu Ile Arg Phe
 370 375 380
 Gly Ser Lys Val Pro Gly Ser Ala Met Glu Val Arg Asp Val Asn Met
 385 390 395 400
 20 Asp Phe Ser Tyr Ser Glu Ser Phe Thr Glu Glu Ser Pro Glu Ala Tyr
 405 410 415
 Glu Arg Leu Ile Leu Asp Ala Leu Leu Asp Glu Ser Ser Leu Phe Pro
 420 425 430
 25 Thr Asn Glu Glu Val Glu Leu Ser Trp Lys Ile Leu Asp Pro Ile Leu
 435 440 445
 Glu Ala Trp Asp Ala Asp Gly Glu Pro Glu Asp Tyr Pro Ala Gly Thr
 450 455 460
 30 Trp Gly Pro Lys Ser Ala Asp Glu Met Leu Ser Arg Asn Gly His Thr
 465 470 475 480
 35 Trp Arg Arg Pro

 40 <210> 9
 <211> 2259
 <212> DNA
 <213> *Corynebacterium glutamicum*

 45 <220>
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 <222> (538)..(2079)
 <223> Zwf-Protein

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 55 cgccccagt gggcatccac cggcgtgaag aacctgcgt acgctgcaac tctttacgtt 180
 tccgagctgg ctggtccaaa caccgtcaac accatgccag aaggcaccat cgacgtctgt 240
 ctggaactgg gcaacctgca cggtgacaac ctgtccaact ccgcggcaga agctgacgct 300

	gtgtttctccc	agcttgaggc	tctgggcggt	gacttggcag	atgtcttcca	ggctctggag	360
5	accgaggccg	tggacaagtt	cggtgcttct	tggagcgaac	tgcttgagtc	catggaagct	420
	cgctgaagt	agaatcagca	cgctgcac	gtaacggcga	catgaaatcg	aattagttcg	480
	atcttatgtg	gccgttacac	atctttcatt	aaagaaagga	tcgtgacgct	taccatc	537
10	gtg agc aca aac acg acc ccc tcc agc tgg aca aac cca ctg cgc gac	585					
	Met Ser Thr Asn Thr Thr Pro Ser Ser Trp Thr Asn Pro Leu Arg Asp						
	1 5 10 15						
15	cgc cag gat aaa cga ctc ccc cgc atc gct ggc cct tcc ggc atg gtg	633					
	Pro Gln Asp Lys Arg Leu Pro Arg Ile Ala Gly Pro Ser Gly Met Val						
	20 25 30						
20	atc ttc ggt gtc act ggc gac ttg gct cga aag aag ctg ctc ccc gcc	681					
	Ile Phe Gly Val Thr Gly Asp Leu Ala Arg Lys Lys Leu Leu Pro Ala						
	35 40 45						
25	att tat gat cta gca aac cgc gga ttg ctg ccc cca gga ttc tcg ttg	729					
	Ile Tyr Asp Leu Ala Asn Arg Gly Leu Leu Pro Pro Gly Phe Ser Leu						
	50 55 60						
30	gta ggt tac ggc cgc cgc gaa tgg tcc aaa gaa gac ttt gaa aaa tac	777					
	Val Gly Tyr Gly Arg Glu Trp Ser Lys Glu Asp Phe Glu Lys Tyr						
	65 70 75 80						
35	gta cgc gat gcc gca agt gct ggt gct cgt acg gaa ttc cgt gaa aat	825					
	Val Arg Asp Ala Ala Ser Ala Gly Ala Arg Thr Tyr Phe Arg Glu Asn						
	85 90 95						
40	gtt tgg gag cgc ctc gcc gag ggt atg gaa ttt gtt cgc ggc aac ttt	873					
	Val Trp Glu Arg Leu Ala Glu Gly Met Glu Phe Val Arg Gly Asn Phe						
	100 105 110						
45	gat gat gat gca gct ttc gac aac ctc gct gca aca ctc aag cgc atc	921					
	Asp Asp Asp Ala Ala Phe Asp Asn Leu Ala Ala Thr Leu Lys Arg Ile						
	115 120 125						
50	gac aaa acc cgc ggc acc gcc ggc aac tgg gct tac tac ctg tcc att	969					
	Asp Lys Thr Arg Gly Thr Ala Gly Asn Trp Ala Tyr Tyr Leu Ser Ile						
	130 135 140						
55	cca cca gat tcc ttc gca gcg gtc tgc cac cag ctg gag cgt tcc ggc	1017					
	Pro Pro Asp Ser Phe Ala Ala Val Cys His Gln Leu Glu Arg Ser Gly						
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60	atg gct gaa tcc acc gaa gaa gca tgg cgc cgc gtg atc atc gag aag	1065					
	Met Ala Glu Ser Thr Glu Glu Ala Trp Arg Arg Val Ile Ile Glu Lys						
	165 170 175						
65	cct ttc ggc cac aac ctc gaa tcc gca cac gag ctc aac cag ctg gtc	1113					
	Pro Phe Gly His Asn Leu Glu Ser Ala His Glu Leu Asn Gln Leu Val						
	180 185 190						

	aac gca gtc ttc cca gaa tct tct gtg ttc cgc atc gac cac tat ttg	1161
	Asn Ala Val Phe Pro Glu Ser Ser Val Phe Arg Ile Asp His Tyr Leu	
	195 200 205	
5	ggc aag gaa aca gtt caa aac atc ctg gct ctg cgt ttt gct aac cag	1209
	Gly Lys Glu Thr Val Gln Asn Ile Leu Ala Leu Arg Phe Ala Asn Gln	
	210 215 220	
10	ctg ttt gag cca ctg tgg aac tcc aac tac gtt gac cac gtc cag atc	1257
	Leu Phe Glu Pro Leu Trp Asn Ser Asn Tyr Val Asp His Val Gln Ile	
	225 230 235 240	
15	acc atg gct gaa gat att ggc ttg ggt gga cgt gct ggt tac tac gac	1305
	Thr Met Ala Glu Asp Ile Gly Leu Gly Gly Arg Ala Gly Tyr Asp	
	245 250 255	
20	ggc atc ggc gca gcc cgc gac gtc atc cag aac cac ctg atc cag ctc	1353
	Gly Ile Gly Ala Ala Arg Asp Val Ile Gln Asn His Leu Ile Gln Leu	
	260 265 270	
25	ttg gct ctg gtt gcc atg gaa gaa cca att tct ttc gtg cca gcg cag	1401
	Leu Ala Leu Val Ala Met Glu Glu Pro Ile Ser Phe Val Pro Ala Gln	
	275 280 285	
30	cca ttg gat aaa acc tcc gct cgt ggt cag tac gct gcc ggt tgg cag	1497
	Pro Leu Asp Lys Thr Ser Ala Arg Gly Gln Tyr Ala Ala Gly Trp Gln	
	305 310 315 320	
35	ggc tct gag tta gtc aag gga ctt cgc gaa gaa gat ggc ttc aac cct	1545
	Gly Ser Glu Leu Val Lys Gly Leu Arg Glu Glu Asp Gly Phe Asn Pro	
	325 330 335	
40	gag tcc acc act gag act ttt gcg gct tgt acc tta gag atc acg tct	1593
	Glu Ser Thr Thr Glu Thr Phe Ala Ala Cys Thr Leu Glu Ile Thr Ser	
	340 345 350	
45	cgt cgc tgg gct ggt gtg ccg ttc tac ctg cgc acc ggt aag cgt ctt	1641
	Arg Arg Trp Ala Gly Val Pro Phe Tyr Leu Arg Thr Gly Lys Arg Leu	
	355 360 365	
50	ggt cgc cgt gtt act gag att gcc gtg gtg ttt aaa gac gca cca cac	1689
	Gly Arg Arg Val Thr Glu Ile Ala Val Val Phe Lys Asp Ala Pro His	
	370 375 380	
55	cag cct ttc gac ggc gac atg act gta tcc ctt ggc caa aac gcc atc	1737
	Gln Pro Phe Asp Gly Asp Met Thr Val Ser Leu Gly Gln Asn Ala Ile	
	385 390 395 400	
55	gtg att cgc gtg cag cct gat gaa ggt gtg ctc atc cgc ttc ggt tcc	1785
	Val Ile Arg Val Gln Pro Asp Glu Gly Val Leu Ile Arg Phe Gly Ser	
	405 410 415	
55	aag gtt cca ggt tct gcc atg gaa gtc cgt gac gtc aac atg gac ttc	1833
	Lys Val Pro Glu Ser Ala Met Glu Val Arg Asp Val Asn Met Asp Phe	
	420 425 430	

tcc tac tca gaa tcc ttc act gaa gaa tca cct gaa gca tac gag cgc 1881
 Ser Tyr Ser Glu Ser Phe Thr Glu Glu Ser Pro Glu Ala Tyr Glu Arg
 435 440 445
 5 ctt atc ttg gat gcg ctg ttg gat gaa tcc agc ctt ttc cct acc aac 1929
 Leu Ile Leu Asp Ala Leu Leu Asp Glu Ser Ser Leu Phe Pro Thr Asn
 450 455 460
 10 gag gaa gtg gaa ctg agc tgg aag att ctg gat cca att ctt gaa gca 1977
 Glu Glu Val Glu Leu Ser Trp Lys Ile Leu Asp Pro Ile Leu Glu Ala
 465 470 475 480
 15 tgg gat gcc gat gga gaa cca gag gat tac cca gca ggt acg tgg ggt 2025
 Trp Asp Ala Asp Gly Glu Pro Glu Asp Tyr Pro Ala Gly Thr Trp Gly
 485 490 495
 20 cca aag agc gct gat gaa atg ctt tcc cgc aac ggt cac acc tgg cgc 2073
 Pro Lys Ser Ala Asp Glu Met Leu Ser Arg Asn Gly His Thr Trp Arg
 500 505 510
 agg cca taatttaggg gcaaaaaatg atctttgaac ttccggatac caccaccag 2129
 Arg Pro
 25 caaatttcca agacctaac tcgactgcgt gaatcgggca cccaggtcac caccggccga 2189
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 35 <213> Corynebacterium glutamicum
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 35 40 45
 Ile Tyr Asp Leu Ala Asn Arg Gly Leu Leu Pro Pro Gly Phe Ser Leu
 50 55 60
 50 Val Gly Tyr Gly Arg Arg Glu Trp Ser Lys Glu Asp Phe Glu Lys Tyr
 65 70 75 80
 Val Arg Asp Ala Ala Ser Ala Gly Ala Arg Thr Glu Phe Arg Glu Asn
 85 90 95
 55 Val Trp Glu Arg Leu Ala Glu Gly Met Glu Phe Val Arg Gly Asn Phe
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Asp Asp Asp Ala Ala Phe Asp Asn Leu Ala Ala Thr Leu Lys Arg Ile
 115 120 125
 5 Asp Lys Thr Arg Gly Thr Ala Gly Asn Trp Ala Tyr Tyr Leu Ser Ile
 130 135 140
 Pro Pro Asp Ser Phe Ala Ala Val Cys His Gln Leu Glu Arg Ser Gly
 145 150 155 160
 10 Met Ala Glu Ser Thr Glu Glu Ala Trp Arg Arg Val Ile Ile Glu Lys
 165 170 175
 Pro Phe Gly His Asn Leu Glu Ser Ala His Glu Leu Asn Gln Leu Val
 180 185 190
 15 Asn Ala Val Phe Pro Glu Ser Ser Val Phe Arg Ile Asp His Tyr Leu
 195 200 205
 Gly Lys Glu Thr Val Gln Asn Ile Leu Ala Leu Arg Phe Ala Asn Gln
 210 215 220
 20 Leu Phe Glu Pro Leu Trp Asn Ser Asn Tyr Val Asp His Val Gln Ile
 225 230 235 240
 Thr Met Ala Glu Asp Ile Gly Leu Gly Gly Arg Ala Gly Tyr Tyr Asp
 245 250 255
 Gly Ile Gly Ala Ala Arg Asp Val Ile Gln Asn His Leu Ile Gln Leu
 260 265 270
 30 Leu Ala Leu Val Ala Met Glu Glu Pro Ile Ser Phe Val Pro Ala Gln
 275 280 285
 Leu Gln Ala Glu Lys Ile Lys Val Leu Ser Ala Thr Lys Pro Cys Tyr
 290 295 300
 Pro Leu Asp Lys Thr Ser Ala Arg Gly Gln Tyr Ala Ala Gly Trp Gln
 305 310 315 320
 40 Gly Ser Glu Leu Val Lys Gly Leu Arg Glu Glu Asp Gly Phe Asn Pro
 325 330 335
 Glu Ser Thr Thr Glu Thr Phe Ala Ala Cys Thr Leu Glu Ile Thr Ser
 340 345 350
 45 Arg Arg Trp Ala Gly Val Pro Phe Tyr Leu Arg Thr Gly Lys Arg Leu
 355 360 365
 Gly Arg Arg Val Thr Glu Ile Ala Val Val Phe Lys Asp Ala Pro His
 370 375 380
 50 Gln Pro Phe Asp Gly Asp Met Thr Val Ser Leu Gly Gln Asn Ala Ile
 385 390 395 400
 Val Ile Arg Val Gln Pro Asp Glu Gly Val Leu Ile Arg Phe Gly Ser
 405 410 415
 Lys Val Pro Gly Ser Ala Met Glu Val Arg Asp Val Asn Met Asp Phe
 420 425 430

Ser Tyr Ser Glu Ser Phe Thr Glu Glu Ser Pro Glu Ala Tyr Glu Arg
 435 440 445
 5 Leu Ile Leu Asp Ala Leu Leu Asp Glu Ser Ser Leu Phe Pro Thr Asn
 450 455 460
 Glu Glu Val Glu Leu Ser Trp Lys Ile Leu Asp Pro Ile Leu Glu Ala
 465 470 475 480
 10 Trp Asp Ala Asp Gly Glu Pro Glu Asp Tyr Pro Ala Gly Thr Trp Gly
 485 490 495
 15 Pro Lys Ser Ala Asp Glu Met Leu Ser Arg Asn Gly His Thr Trp Arg
 500 505 510
 Arg Pro
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 35 <210> 12
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